````
---
title: "BIO392-cnv-freq"
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date: "28.09.22"
output:
  pdf_document: default
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```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```

## Step 1: Install package

```{r}
install.packages("devtools")
```

```{r}
devtools::install_github("progenetix/pgxRpi")
```

```{r}
library(pgxRpi)
```

## Step2: Search esophageal adenocarcinoma NCIt code C4025

## Step3: Access the CNV frequency data from samples with esophageal adenocarcinoma

```{r}
freq <- pgxLoader(type='frequency', output='pgxseg',filters='NCIT:C3058', codematches=T)
```

### The retreived data is an object contaning two slots `meta` and `data`.

The `meta` slot looks like this:

```{r}
freq$meta
```

The `data` slot includes two matrices.

```{r}
names(freq$data)
```

The frequency matrix looks like this

```{r}
head(freq$data$`NCIT:C3058`)
```

Dimension of this matrix
````

```{r}
dim(freq$data$`NCIT:C3058`)
```

Step4: Visualize data

By genome

```{r,fig.width=12,fig.height=6}
pgxFreqplot(freq)
```

By chromosome

```{r,fig.width=12, fig.height=6}
pgxFreqplot(freq,chrom = 20)
```

Step5: Analyse the data

According the plot, we can see frequenct gains on chromosome 7p, 8q, 20p, 20q
and frequenct losses on chromosome 4p,4q, 5q, 9p, 17p, 18q, 21q.

There is a literature where the findings are consistent with the majority of mine. Here is the [paper-link](https://www.nature.com/articles/modpathol2008150).

A more detailed use case see this [link](https://htmlpreview.github.io/?https://github.com/progenetix/pgxRpi/blob/main/vignettes/Introduction_2_loadfrequency.html).